RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/537, 767 ___

Source: _____ IFWO, ___

Date Processed by STIC: _____ 05/18/2006 ___

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 05/18/2006
PATENT APPLICATION: US/10/537,767   TIME: 13:47:13

Input Set : A:\10-537,767 Sequence Listing.txt
Output Set: N:\CRF4\05182006\J537767.raw

```
 3 <110> APPLICANT: Astellas Pharma Inc.
 5 <120> TITLE OF INVENTION: Protein Which Binds To Akt2
 7 <130> FILE REFERENCE: Q88255
 9 <140> CURRENT APPLICATION NUMBER: 10/537,767
10 <141> CURRENT FILING DATE: 2005-06-06
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/15546
13 <151> PRIOR FILING DATE: 2003-12-04
15 <150> PRIOR APPLICATION NUMBER: JP 2002-354155
16 <151> PRIOR FILING DATE: 2002-12-05
18 <150> PRIOR APPLICATION NUMBER: JP 2003-206952
19 <151> PRIOR FILING DATE: 2003-08-08
21 <160> NUMBER OF SEQ ID NOS: 27
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1722
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus sp.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1719)
35 <400> SEQUENCE: 1
36 atg gca gct gtg ccg ccc ctg cgg gac cgc ttg agc ttc ttg cat agg    48
37 Met Ala Ala Val Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
38 1               5                   10                  15
40 ctc ccc atc ctg ttg aag ggg acc tca gat gat agc atc cca tgt cca    96
41 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Ser Ile Pro Cys Pro
42              20                  25                  30
44 ggc tac ctg ttt gaa gag atc gcc aag att tcc cac gag tca cta ggc   144
45 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
46          35                  40                  45
48 agc agc cag tgc ctg ctg gag tac ctc ctg aac cgt ctg gac agc agc   192
49 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser
50      50                  55                  60
52 tcc ggc cac gtg aag ctc aag gtg cta aag atc ttg ctt tac ctg tgt   240
53 Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
54 65                  70                  75                  80
56 ggt cat ggc tct tcc tcc ttc ctc ctc atc ctc agg aga aac tct gct   288
57 Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
58                  85                  90                  95
60 ctc atc caa gaa gcc acg gct ttc tca ggg cct cca gat cct ctt cac   336
61 Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
62              100                 105                 110
64 gga aat agc ttg tac cag aag gtg cgg gcg gct gcc cag gac ctg ggt   384
```

RAW SEQUENCE LISTING   DATE: 05/18/2006
PATENT APPLICATION: US/10/537,767   TIME: 13:47:13

Input Set : A:\10-537,767 Sequence Listing.txt
Output Set: N:\CRF4\05182006\J537767.raw

```
 65 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
 66         115                 120                 125
 68 agc acc ctg ttc tca gat gcc gtg cca cag cct cca tcg cag cca cct     432
 69 Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro
 70     130                 135                 140
 72 cag atc ccg cct ccc gca ggc atg ggc gcc cag gcc aga cct ctt agt     480
 73 Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
 74 145                 150                 155                 160
 76 gcc ctg caa ggc ttc ggc tac acg aag gag agc agc cgg aca ggc tcc     528
 77 Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
 78         165                 170                 175
 80 gca ggt gaa acc ttc ctc tcc acc atc cag agg gcc gca gag gta gtg     576
 81 Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
 82         180                 185                 190
 84 gct aat gct gtg cgt cct gga cct gat aat cct tgt acc aag gga ccc     624
 85 Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
 86         195                 200                 205
 88 ttg ccg tat ggt gat tcc tac cag cct gca gtg aca cct tca gct agc     672
 89 Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
 90     210                 215                 220
 92 cac aca cat ccc aac cct ggg aat cta ctc cct ggg gcc atc ctg ggg     720
 93 His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
 94 225                 230                 235                 240
 96 gcc aga gct gtg aga cac cag ccc ggg cag gct ggg ggc ggc tgg gat     768
 97 Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
 98         245                 250                 255
100 gag ctg gac agc agt cct agt tcc cag aat tcc tcc tgc acc agc aac     816
101 Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
102         260                 265                 270
104 ctg agc agg gcc tcg gac tcg ggc agt cgg tct ggc agt gac agc cac     864
105 Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His
106         275                 280                 285
108 tct ggc acc agc cgg gag cca ggc gac ctg gca gaa agg gct gag gcc     912
109 Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
110     290                 295                 300
112 acg ccc cca aat gac tgc cag caa gaa ctg aat cta gtg agg act gtg     960
113 Thr Pro Pro Asn Asp Cys Gln Gln Glu Leu Asn Leu Val Arg Thr Val
114 305                 310                 315                 320
116 aca cag ggg cca cgt gtc ttc ctg agc cgt gag gag acg cag cac ttc    1008
117 Thr Gln Gly Pro Arg Val Phe Leu Ser Arg Glu Glu Thr Gln His Phe
118         325                 330                 335
120 atc aaa gag tgt ggc ctg ctc aac tgt gag gca gtg ctg gag ctg ctc    1056
121 Ile Lys Glu Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Glu Leu Leu
122         340                 345                 350
124 ctg cgc cag ctg gtc ggg acc agt gag tgc gag cag atg agg gcg ctg    1104
125 Leu Arg Gln Leu Val Gly Thr Ser Glu Cys Glu Gln Met Arg Ala Leu
126         355                 360                 365
128 tgt gcc atc gcg tcc ttt ggg agt gct gac ctc ctg cct cag gag cac    1152
129 Cys Ala Ile Ala Ser Phe Gly Ser Ala Asp Leu Leu Pro Gln Glu His
```

```
130      370                375                380
132 gtc ctc ctc ctg tgc cga cag cag ctg cag gaa ctt ggc gcg ggc agc      1200
133 Val Leu Leu Leu Cys Arg Gln Gln Leu Gln Glu Leu Gly Ala Gly Ser
134 385                390                395                400
136 cct gga cct gtg acc aac aaa gcc acc aag atc ctg aga cat ttt gaa      1248
137 Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe Glu
138                405                410                415
140 gcc tcc tgt gga caa cag ctc cct acc cta agg ctc tgt gcc cag ccc      1296
141 Ala Ser Cys Gly Gln Gln Leu Pro Thr Leu Arg Leu Cys Ala Gln Pro
142                420                425                430
144 aac tct gca gct gcc cct gtg ggc cca gct gac ctg ctg acc agc ccc      1344
145 Asn Ser Ala Ala Ala Pro Val Gly Pro Ala Asp Leu Leu Thr Ser Pro
146                435                440                445
148 gtg cct gcc cct ggg agc cag gtc tgc ctc cag cct ctc agc tcc gcc      1392
149 Val Pro Ala Pro Gly Ser Gln Val Cys Leu Gln Pro Leu Ser Ser Ala
150      450                455                460
152 aca gtg gta ccc agg agt cct gtg ctc ttt cca tcc ccc aat acc tta      1440
153 Thr Val Val Pro Arg Ser Pro Val Leu Phe Pro Ser Pro Asn Thr Leu
154 465                470                475                480
156 cct ccg tct gct ctg gag gag ccc agc gag gtc cga acc caa ttg gtg      1488
157 Pro Pro Ser Ala Leu Glu Glu Pro Ser Glu Val Arg Thr Gln Leu Val
158                485                490                495
160 tgt tct agt gaa cag ggg aca gaa tct gag cag agg ctg gag aac aca      1536
161 Cys Ser Ser Glu Gln Gly Thr Glu Ser Glu Gln Arg Leu Glu Asn Thr
162                500                505                510
164 gac acc cca gag gat agc tcc agt ccg ctc ccg tgg agt ccc aac tct      1584
165 Asp Thr Pro Glu Asp Ser Ser Ser Pro Leu Pro Trp Ser Pro Asn Ser
166                515                520                525
168 ttg ttt gct ggc atg gag ctg gtg gct tgc ccc cgc ctg cct tgc cac      1632
169 Leu Phe Ala Gly Met Glu Leu Val Ala Cys Pro Arg Leu Pro Cys His
170      530                535                540
172 agc tcg cag gac ctc cag aca gat tta cag aag gtg acc aca gaa gct      1680
173 Ser Ser Gln Asp Leu Gln Thr Asp Leu Gln Lys Val Thr Thr Glu Ala
174 545                550                555                560
176 ccg gtt tca gag cca tca gct ttt gca ttt tta aac atg tga            1722
177 Pro Val Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn Met
178                565                570
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 573
183 <212> TYPE: PRT
184 <213> ORGANISM: Mus sp.
186 <400> SEQUENCE: 2
188 Met Ala Ala Val Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
189 1                5                10                15
192 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Ser Ile Pro Cys Pro
193                20                25                30
196 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Leu Gly
197      35                40                45
200 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Asn Arg Leu Asp Ser Ser
```

```
201     50                      55                  60
204 Ser Gly His Val Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
205 65                      70                  75                  80
208 Gly His Gly Ser Ser Ser Phe Leu Leu Ile Leu Arg Arg Asn Ser Ala
209                 85                  90                  95
212 Leu Ile Gln Glu Ala Thr Ala Phe Ser Gly Pro Pro Asp Pro Leu His
213             100                 105                 110
216 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
217         115                 120                 125
220 Ser Thr Leu Phe Ser Asp Ala Val Pro Gln Pro Pro Ser Gln Pro Pro
221     130                 135                 140
224 Gln Ile Pro Pro Pro Ala Gly Met Gly Ala Gln Ala Arg Pro Leu Ser
225 145                 150                 155                 160
228 Ala Leu Gln Gly Phe Gly Tyr Thr Lys Glu Ser Ser Arg Thr Gly Ser
229                 165                 170                 175
232 Ala Gly Glu Thr Phe Leu Ser Thr Ile Gln Arg Ala Ala Glu Val Val
233             180                 185                 190
236 Ala Asn Ala Val Arg Pro Gly Pro Asp Asn Pro Cys Thr Lys Gly Pro
237         195                 200                 205
240 Leu Pro Tyr Gly Asp Ser Tyr Gln Pro Ala Val Thr Pro Ser Ala Ser
241     210                 215                 220
244 His Thr His Pro Asn Pro Gly Asn Leu Leu Pro Gly Ala Ile Leu Gly
245 225                 230                 235                 240
248 Ala Arg Ala Val Arg His Gln Pro Gly Gln Ala Gly Gly Gly Trp Asp
249                 245                 250                 255
252 Glu Leu Asp Ser Ser Pro Ser Ser Gln Asn Ser Ser Cys Thr Ser Asn
253             260                 265                 270
256 Leu Ser Arg Ala Ser Asp Ser Gly Ser Arg Ser Gly Ser Asp Ser His
257         275                 280                 285
260 Ser Gly Thr Ser Arg Glu Pro Gly Asp Leu Ala Glu Arg Ala Glu Ala
261     290                 295                 300
264 Thr Pro Pro Asn Asp Cys Gln Gln Glu Leu Asn Leu Val Arg Thr Val
265 305                 310                 315                 320
268 Thr Gln Gly Pro Arg Val Phe Leu Ser Arg Glu Glu Thr Gln His Phe
269             325                 330                 335
272 Ile Lys Glu Cys Gly Leu Leu Asn Cys Glu Ala Val Leu Glu Leu Leu
273             340                 345                 350
276 Leu Arg Gln Leu Val Gly Thr Ser Glu Cys Glu Gln Met Arg Ala Leu
277         355                 360                 365
280 Cys Ala Ile Ala Ser Phe Gly Ser Ala Asp Leu Leu Pro Gln Glu His
281     370                 375                 380
284 Val Leu Leu Leu Cys Arg Gln Gln Leu Gln Glu Leu Gly Ala Gly Ser
285 385                 390                 395                 400
288 Pro Gly Pro Val Thr Asn Lys Ala Thr Lys Ile Leu Arg His Phe Glu
289             405                 410                 415
292 Ala Ser Cys Gly Gln Gln Leu Pro Thr Leu Arg Leu Cys Ala Gln Pro
293         420                 425                 430
296 Asn Ser Ala Ala Ala Pro Val Gly Pro Ala Asp Leu Leu Thr Ser Pro
297         435                 440                 445
```

```
                    RAW SEQUENCE LISTING              DATE: 05/18/2006
                    PATENT APPLICATION:  US/10/537,767   TIME: 13:47:13

                    Input Set : A:\10-537,767 Sequence Listing.txt
                    Output Set: N:\CRF4\05182006\J537767.raw

300 Val Pro Ala Pro Gly Ser Gln Val Cys Leu Gln Pro Leu Ser Ser Ala
301     450                 455                 460
304 Thr Val Val Pro Arg Ser Pro Val Leu Phe Pro Ser Pro Asn Thr Leu
305 465                 470                 475                 480
308 Pro Pro Ser Ala Leu Glu Glu Pro Ser Glu Val Arg Thr Gln Leu Val
309                 485                 490                 495
312 Cys Ser Ser Glu Gln Gly Thr Glu Ser Glu Gln Arg Leu Glu Asn Thr
313                 500                 505                 510
316 Asp Thr Pro Glu Asp Ser Ser Ser Pro Leu Pro Trp Ser Pro Asn Ser
317         515                 520                 525
320 Leu Phe Ala Gly Met Glu Leu Val Ala Cys Pro Arg Leu Pro Cys His
321         530                 535                 540
324 Ser Ser Gln Asp Leu Gln Thr Asp Leu Gln Lys Val Thr Thr Glu Ala
325 545                 550                 555                 560
328 Pro Val Ser Glu Pro Ser Ala Phe Ala Phe Leu Asn Met
329                 565                 570
332 <210> SEQ ID NO: 3
333 <211> LENGTH: 1782
334 <212> TYPE: DNA
335 <213> ORGANISM: Homo sapiens
338 <220> FEATURE:
339 <221> NAME/KEY: CDS
340 <222> LOCATION: (1)..(1782)
342 <400> SEQUENCE: 3
343 atg gct gcc gcg ccg ccg cta cgg gac cgc ctg agc ttt cta cac cgg       48
344 Met Ala Ala Ala Pro Pro Leu Arg Asp Arg Leu Ser Phe Leu His Arg
345 1               5                   10                  15
347 ctc ccg att ctc ctg aag ggg acg tcc gat gat gat gtc ccg tgt ccg       96
348 Leu Pro Ile Leu Leu Lys Gly Thr Ser Asp Asp Asp Val Pro Cys Pro
349             20                  25                  30
351 ggc tac ctg ttt gaa gag att gct aaa atc tcc cac gag tct ccg ggc      144
352 Gly Tyr Leu Phe Glu Glu Ile Ala Lys Ile Ser His Glu Ser Pro Gly
353         35                  40                  45
355 agc agc cag tgc ctg ctg gag tac ctc ctg agc cgc ctg cac agc agc      192
356 Ser Ser Gln Cys Leu Leu Glu Tyr Leu Leu Ser Arg Leu His Ser Ser
357     50                  55                  60
359 tcc ggc cac ggg aag ctc aag gtg ctg aag atc ctg ctc tat ctg tgc      240
360 Ser Gly His Gly Lys Leu Lys Val Leu Lys Ile Leu Leu Tyr Leu Cys
361 65                  70                  75                  80
363 agc cac ggc tcc tcc ttc ttc ctg ctc atc ctc aaa cgc aac tct gcc      288
364 Ser His Gly Ser Ser Phe Phe Leu Leu Ile Leu Lys Arg Asn Ser Ala
365             85                  90                  95
367 ttc atc cag gaa gct gca gct ttt gca ggg ccc cca gat cct ctg cac      336
368 Phe Ile Gln Glu Ala Ala Ala Phe Ala Gly Pro Pro Asp Pro Leu His
369             100                 105                 110
371 ggg aac agc ttg tac cag aag gtt cgc gcg gcc gcg cag gac ttg ggg      384
372 Gly Asn Ser Leu Tyr Gln Lys Val Arg Ala Ala Ala Gln Asp Leu Gly
373             115                 120                 125
375 agc acc ctg ttc tcg gac acc gtg ttg ccg ctg gct ccc tcc cag cct      432
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/537,767**

DATE: 05/18/2006
TIME: 13:47:14

Input Set : **A:\10-537,767 Sequence Listing.txt**
Output Set: **N:\CRF4\05182006\J537767.raw**